

AMENDMENTS TO THE CLAIMS

1-53. Canceled

54. (Currently amended) The method of claim 42, A method for predicting a human breast cancer patient as having a good prognosis or a poor prognosis, comprising:

(a) classifying said breast cancer patient into one of the following classes:

(a1) ER⁻ and sporadic;

(a2) ER⁻ and BRCA1;

(a3) ER⁺ and ER/AGE high;

(a4) ER⁺, ER/AGE low and LN⁺; or

(a5) ER⁺, ER/AGE low and LN⁻;

wherein ER⁺ designates a high ER level and ER⁻ designates a low ER level, wherein said ER/AGE is a metric of said ER level relative to the age of said patient, and wherein LN⁺ designates a greater than 0 lymph nodes status in said patient and LN⁻ designates a 0 lymph nodes status in said patient, and wherein said ER/AGE is classified as high if said ER level is greater than $c \cdot (\text{AGE} - d)$, and wherein said ER/AGE is classified as low if said ER level is equal to or less than $c \cdot (\text{AGE} - d)$, wherein c is a coefficient, AGE is the age of said patient, and d is an age threshold;

(b) determining a profile comprising measurements of levels of transcripts of, or proteins encoded by, respective genes in a plurality of genes in a cell sample taken from said breast cancer patient, said respective genes comprising:

(b1) at least five of the genes for which markers are listed in Table 1 if said breast cancer patient is classified as ER⁻ and sporadic;

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(b2) at least two of the genes for which markers are listed in Table 2 if said breast cancer patient is classified as ER⁻ and BRCAl;

(b3) at least two of the genes for which markers are listed in Table 3 if said breast cancer patient is classified as ER+ and ER/AGE high;

(b4) at least two of the genes for which markers are listed in Table 4 if said breast cancer patient is classified as ER+, ER/AGE low and LN+; or

(b5) at least two of the genes for which markers are listed in Table 5 if said breast cancer patient is classified as ER+, ER/AGE low and LN-; and

(c) comparing, on a computer, said profile to a good prognosis template and/or a poor prognosis template, wherein said good prognosis template comprises measurements of average levels of transcripts of, or proteins encoded by, said respective genes a plurality of good outcome patients, and said poor prognosis template comprises measurements of average levels of transcripts of, or proteins encoded by, said respective genes in a plurality of poor outcome patients, and wherein a good outcome patient is a breast cancer patient who has non-reoccurrence of metastases within a first period of time after initial diagnosis and a poor outcome patient is a patient who has reoccurrence of metastases within a second period of time after initial diagnosis; and

(d) classifying said breast cancer patient (i) as having a good prognosis if said profile has a high similarity to said good prognosis template, has a low similarity to said poor prognosis template, or has a higher similarity to said good prognosis template than to said poor prognosis template, wherein said profile has a high similarity to said good prognosis template if the similarity to said good prognosis template is above a predetermined threshold, or has a low similarity to said poor prognosis template if the similarity to said poor prognosis template is below said predetermined threshold, or (ii) as having a poor prognosis if said profile has a high

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similarity to said poor prognosis template, has a low similarity to said good prognosis template, or has a higher similarity to said poor prognosis template than to said good prognosis template, wherein said profile has a high similarity to said poor prognosis template if the similarity to said poor prognosis template is above said predetermined threshold, or has a low similarity to said good prognosis template if the similarity to said good prognosis template is below said predetermined threshold.

55-57. (Canceled)

58. (Currently amended) The method of claim [[42]] 54, wherein said individual is ER⁻ and sporadic, and said plurality of genes comprises at least [[two]] ten of the genes for which markers are listed in Table 1.

59. (Currently amended) The method of claim [[42]] 54, wherein said individual is ER⁻ and sporadic, and said plurality of genes comprises all of the genes for which markers are listed in Table 1.

60. (Currently amended) The method of claim [[42]] 54, wherein said individual is ER⁻ and *BRCA1*, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 2.

61. (Currently amended) The method of claim [[42]] 54, wherein said individual is ER⁻ and *BRCA1*, and said plurality of genes comprises all of the genes for which markers are listed in Table 2

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62. (Currently amended) The method of claim [[42]] 54, wherein said individual is ER+ and ER/AGE high, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 3.

63. (Currently amended) The method of claim [[42]] 54, wherein said individual is ER+ and ER/AGE high, and said plurality of genes comprises all of the genes for which markers are listed in Table 3.

64. (Currently amended) The method of claim [[42]] 54, wherein said individual is ER+, ER/AGE low and LN+, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 4.

65. (Currently amended) The method of claim [[42]] 54, wherein said individual is ER+, ER/AGE low and LN+, and said plurality of genes comprises all of the genes for which markers are listed in Table 4.

66. (Currently amended) The method of claim [[42]] 54, wherein said individual is ER+, ER/AGE low and LN⁻, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 5.

67. (Currently amended) The method of claim [[42]] 54, wherein said individual is ER+, ER/AGE low and LN⁻, and said plurality of genes comprises all of the genes for which markers are listed in Table 5.

68-93. (Canceled)

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94. (Currently amended) ~~The method of claim 89, A computer-implemented method for predicting a human breast cancer patient as having a good prognosis or a poor prognosis, comprising:~~

(a) classifying, on a computer, said patient as having a good prognosis or a poor prognosis based on a profile comprising measurements of levels of transcripts of, or proteins encoded by, respective genes in a plurality of genes in a cell sample taken from said patient, said plurality of genes comprising:

(b1) at least five of the genes for which markers are listed in Table 1 if said patient is ER- and sporadic;

(b2) at least two of the genes for which markers are listed in Table 2 if said patient is ER- and BRCA1;

(b3) at least two of the genes for which markers are listed in Table 3 if said patient is ER+ and ER/AGE high;

(b4) at least two of the genes for which markers are listed in Table 4 if said patient is ER+, ER/AGE low and LN+; or

(b5) at least two of the genes for which markers are listed in Table 5 if said patient is ER+, ER/AGE low and LN-,

wherein ER+ designates a high ER level and ER- designates a low ER level, wherein said ER/AGE is a metric of said ER level relative to the age of said patient, wherein LN+ designates a greater than 0 lymph nodes status in said patient and LN- designates a 0 lymph nodes status in patient, and wherein said ER/AGE is classified as high if said ER level is greater than $c \cdot (AGE - d)$, and wherein said ER/AGE is classified as low if said ER level is equal to or less than $c \cdot (AGE - d)$, wherein c is a coefficient, AGE is the age of said patient, and d is an age threshold,

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wherein said classifying is carried out by a method comprising comparing said profile to a good prognosis template and/or a poor prognosis template, wherein said good prognosis template comprises measurements of average levels of transcripts of, or proteins encoded by, said respective genes in a plurality of good outcome patients, and said poor prognosis template comprises measurements of average levels of transcripts of, or proteins encoded by, said respective genes in a plurality of poor outcome patients, and wherein a good outcome patient is a breast cancer patient who has non-reoccurrence of metastases within a first period of time after initial diagnosis and a poor outcome patient is a breast cancer patient who has reoccurrence of metastases within a second period of time after initial diagnosis, and wherein:

(i) said individual is classified as having a good prognosis if said profile has a high similarity to said good prognosis template, has a low similarity to said poor prognosis template, or has a higher similarity to said good prognosis template than to said poor prognosis template, wherein said profile has a high similarity to said good prognosis template if the similarity to said good prognosis template is above a predetermined threshold, or has a low similarity to said poor prognosis template if the similarity to said poor prognosis template is below said predetermined threshold, or

(ii) said individual is classified as having a poor prognosis if said profile has a high similarity to said poor prognosis template, has a low similarity to said good prognosis template, or has a higher similarity to said poor prognosis template than to said good prognosis template, wherein said profile has a high similarity to said poor prognosis template if the similarity to said poor prognosis template is above said predetermined threshold, or has a low similarity to said good prognosis template if the similarity to said good prognosis template is below said predetermined threshold.

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95. (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER- and sporadic, and said plurality of genes comprises at least ten two of the genes for which markers are listed in Table 1.

96. (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER- and sporadic, and said plurality of genes comprises all of the genes for which markers are listed in Table 1.

97. (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER- and *BRCA1*, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 2.

98. (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER- and *BRCA1*, and said plurality of genes comprises all of the genes for which markers are listed in Table 2.

99. (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER+ and ER/AGE high, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 3.

100. (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER+ and ER/AGE high, and said plurality of genes comprises all of the genes for which markers are listed in Table 3.

101. (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER+; ER/AGE low and LN+, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 4.

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102. (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER+, ER/AGE low and LN+, and said plurality of genes comprises all of the genes for which markers are listed in Table 4.

103. (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER+, ER/AGE low and LN⁻, and said plurality of genes comprises at least [[two]] five of the genes for which markers are listed in Table 5.

104. (Currently amended) The method of claim [[89]] 94, wherein said individual has been classified as ER+, ER/AGE low and LN⁻, and said plurality of genes comprises all of the genes for which markers are listed in Table 5.

105. (Canceled)

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